

SEQUENCE LISTING

<110> Thompson, M. Craig  
Long, Fan  
Wobbe, C. Richard

<120> A NOVEL FUNGAL MULTISUBUNIT PROTEIN  
COMPLEX CRITICAL FOR EXPRESSION OF FUNGAL PROTEINS

<130> 0342/1D516US2

<140> TBA

<141> Concurrently Herewith

<150> PCT/US99/02940

<151> 1999-02-08

<150> 60/074,100

<151> 1998-02-09

<160> 32

<170> FastSEQ for Windows Version 3.0

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<211> 4116

<212> DNA

<213> C. albicans

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Gln	Lys	Gln	Gln	Leu	Asp	Ser	Ser	Asn	Leu	Ile	Leu	Pro	Leu	Asn	Glu	
			420					425					430			

Thr	Ile	Leu	Gln	Gln	Lys	Phe	Asn	Leu	Ser	Asn	Asp	Asp	Lys	Tyr	Gln
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Ile	Leu	Lys	Lys	Thr	His	Gln	Thr	Lys	Val	Arg	Ser	Thr	Ile	Ser	Asn
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Tyr	Lys	Val	Ala	Val	Pro	Arg	Tyr	Gln	Leu	Arg	His	Phe	His	Arg	Glu
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			500					505					510		
Leu	Lys	Ala	Arg	Lys	Arg	Lys	Arg	Asp	Lys	Gly	Lys	Asp	Val	Lys	Glu
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Gly	Met	Ala	Asn	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Ala	Asn	Glu	Gln
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His	Ile	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Ile	Arg	Ala	Pro	Val	Phe
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Phe	Gly	Ile	Ser	Asn	Arg	Phe	Tyr	Leu	Arg	Asn	Ile	Asn	His	Leu	Phe
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Thr	Val	Gly	Gln	Thr	Phe	Pro	Val	Glu	Glu	Ile	Pro	Gly	Pro	Asn	Ser
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Lys	Glu	Phe	Met	Lys	Tyr	Gln	Arg	Asp	Gly	Pro	Glu	Lys	Gly	Leu	Trp
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		755					760					765			
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Ile	Asn	Ser	Thr	Gln	Met	Arg	Ala	Met	Ile	Gln	Ile	His	Gly	Val	Gly
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Lys	Ser	Leu	Ser	Ile	Ser	Asn	Pro	Phe	Glu	Glu	Met	Thr	Asn	Pro	Asp
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Glu	Ile	Asn	Gln	Thr	Asn	Lys	His	Val	Lys	Thr	Asp	Arg	Asp	Asp	Lys
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Cys	Gly	Gln	Ile	Gly	His	Ile	Arg	Thr	Asn	Lys	Ser	Cys	Pro	Met	Tyr
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 <212> PRT  
 <213> S. pombe

<400> 4

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Asp	Met	Ser	Val	Ile	Asn	Ser	Leu	Leu	Gly	Asp	Thr	Asn	Asn	Pro	Gly
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Met	Asn	Glu	Ser	Pro	Lys	Ile	Leu	Asp	Ser	Ser	Phe	Glu	Asn	Ser	Asn
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Pro	Gln	Asp	Gly	Pro	Asn	Tyr	Glu	Asp	Phe	Asp	Phe	Met	Gly	Ser	Ile
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His	Lys	Glu	Phe	Gly	Asn	Asn	Ile	Asn	Glu	Met	Asp	Asp	Met	Glu	Asp
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Gly	Asp	Lys	Asp	Asp	Glu	Asp	Phe	Gly	Lys	Leu	Leu	Ala	Lys	Glu	Met
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Gly	Glu	Glu	Ala	Ala	Gly	Gln	Val	Leu	Ser	Gly	Val	Gly	Phe	Ser	Ile



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	Lys	Thr	Phe	Phe	Pro	180	Thr	Phe	Glu	Arg	Gly	Val	Leu	Leu	Asn	Phe	Ser
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385					405										395		400
	Pro	Tyr	Tyr	Lys	Thr	410	Arg	Leu	Ser	Lys	Arg	Ala	Val	Arg	Ser	Tyr	His
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465					485										475		480
	Gly	Met	Ala	Ser	Arg	490	Ile	Val	Asn	Tyr	Tyr	Arg	Lys	Lys	Asn	Glu	Gln
					500										495		
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	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly	Val			
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	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu	Ile	Asn			
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	Ile	Thr	Thr	Arg	Asn	Phe	Ile	Asn	Ala	Thr	Gln	Gly	Lys	Ala	Met	Leu			
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	Phe	Ile	Arg	Thr	Ser	Met	Lys	Gly	Gly	Phe	Lys	Pro	Ala	Gly	Glu	Thr			
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	Ala	Asp	Asp	Lys	Pro	Glu	Pro	Gln	Thr	Lys	Asn	Ala	His	Ala	Tyr	Asn			
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	Glu	Glu	Thr	Thr	Arg	Glu	Glu	Thr	Pro	Ser	Ser	Asp	Lys	Val	Leu	Arg			
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	Arg	Glu	Ile	Asp	Glu	Gln	Ser	Thr	Ala	Leu	Asp	Ala	Val	Val	Pro	Thr			
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	Gly	Asp	Glu	Ala	Ile	Asp	Arg	Arg	Asn	Arg	Arg	Arg	Leu	Glu	Gln	Glu			
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Asp Lys Asn

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Leu	Gln	Asp	Asp	Asp	Gly	Glu	Gly	Arg	Gly	Gly	Thr	Gly	Phe	Asp	Ala
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65					70					75					80
Asp	Glu	Glu	Glu	Glu	Asp	Ala	Arg	Pro	Ser	Ala	Val	Ser	Ala	Ser	Gly
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Thr	Ser	Thr	Tyr	Asp	Asp	Leu	Glu	Asp	Ala	Ile	Pro	Ala	Ser	Lys	Val
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Glu	Ala	Lys	Leu	Thr	Lys	Asp	Asp	Lys	Glu	Leu	Met	Pro	Pro	Pro	Ser
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Ala	Pro	Met	Arg	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Glu	Glu	Pro	Ala	Lys
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Ser	Asn	Asp	Ala	Ser	Ser	Pro	Ser	Asp	Asp	Ser	Lys	Ser	Thr	Asp	Ser
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Lys	Asp	Ala	Asp	Arg	Lys	Leu	Asp	Thr	Pro	Leu	Ala	Asp	Ile	Leu	Pro
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Pro	Gln	Lys	Val	Leu	Arg	Phe	Ser	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Pro
				245					250					255	
Thr	Ser	Leu	Pro	Gln	Ile	Trp	Arg	His	Val	Arg	Lys	Arg	Arg	Arg	Lys
			260					265					270		
Arg	Asn	Gln	Ser	Arg	Asp	Gln	Lys	Thr	Thr	Asn	Thr	Gly	Gly	Ser	Asp
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	290					295					300				
Tyr	Ala	Ala	Glu	Pro	Thr	Pro	Ala	Glu	Cys	Met	Ser	Asp	Asp	Glu	Asp
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Lys	Leu	Leu	Gly	Asp	Phe	Asn	Ser	Glu	Asp	Val	Arg	Pro	Glu	Gly	Pro
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Val	Lys	Lys	Ser	Lys	Ile	Leu	Leu	Gly	Lys	Ala	Gly	Val	Ile	Asn	Val		
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Leu	Ala	Glu	Asp	Thr	Pro	Pro	Pro	Pro	Pro	Lys	Ser	Pro	Asp	Arg	Asp		
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Pro	Phe	Asn	Ile	Ser	Asn	Asp	Thr	Tyr	Tyr	Thr	Pro	Lys	Thr	Glu	Pro		
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Thr	Leu	Arg	Leu	Lys	Val	Gly	Gly	Asn	Leu	Ile	Gln	His	Ser	Thr	Pro		
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Val	Val	Glu	Leu	Arg	Ala	Pro	Phe	Val	Pro	Thr	His	Met	Gly	Pro	Met		
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Asn	Val	Arg	Ala	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	His	Gly		
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Ile	Ala	Lys	Lys	Ala	Lys	Gln	Arg	Glu	Val	Glu	Arg	Ile	Ala	Ser	Gly		
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Lys	Ala	Glu	Lys	Asp	Ser	Gly	Pro	Gln	Asp	Tyr	Val	Tyr	Gly	Glu	Val
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His	Lys	Met	Ala	His	Asn	Asp	Phe	Leu	Val	Ile	Arg	Thr	Arg	Asn	Asn
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Thr	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe	Trp	Lys	Ser
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Arg	Asp	Asn	Pro	Arg	Arg	Ile	Arg	Met	Asp	Asp	Ile	Lys	Gln	Ala	Phe
865					870					875					880
Pro	Ala	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys	Gln	Cys	Ala
				885					890					895	
Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val	Ile	Lys	Pro
			900					905					910		
Glu	Phe	Arg	Leu	Pro	Ser	Glu	Glu	Glu	Ile	Arg	Ala	Met	Val	Ser	Pro
		915					920					925			
Glu	Gln	Cys	Cys	Ala	Tyr	Phe	Ser	Met	Ile	Ala	Ala	Glu	Gln	Arg	Leu
	930					935					940				
Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Phe	Leu	Phe	Ala	Pro	Gln	Glu	Asp
945					950					955					960
Asp	Asp	Glu	Glu	Ala	Gln	Leu	Lys	Leu	Asp	Asp	Glu	Val	Lys	Val	Ala
				965					970					975	
Pro	Trp	Asn	Thr	Thr	Arg	Ala	Tyr	Ile	Gln	Ala	Met	Arg	Gly	Lys	Cys
			980					985					990		
Leu	Leu	Gln	Leu	Ser	Gly	Pro	Ala	Asp	Pro	Thr	Gly	Cys	Gly	Glu	Gly
		995				1000						1005			
Phe	Ser	Tyr	Val	Arg	Val	Pro	Asn	Lys	Pro	Thr	Gln	Thr	Lys	Glu	Glu
	1010					1015					1020				
Gln	Glu	Ser	Gln	Pro	Lys	Arg	Ser	Val	Thr	Gly	Thr	Asp	Ala	Asp	Leu
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Arg	Arg	Leu	Pro	Leu	Gln	Arg	Ala	Lys	Glu	Leu	Leu	Arg	Gln	Phe	Lys
				1045					1050					1055	
Val	Pro	Glu	Glu	Glu	Ile	Lys	Lys	Leu	Ser	Arg	Trp	Glu	Val	Ile	Asp
			1060					1065					1070		
Val	Val	Arg	Thr	Leu	Ser	Thr	Glu	Lys	Ala	Lys	Ala	Gly	Glu	Glu	Gly
		1075					1080					1085			
Met	Asp	Lys	Phe	Ser	Arg	Gly	Asn	Arg	Phe	Ser	Ile	Ala	Glu	His	Gln
	1090					1095					1100				
Glu	Arg	Tyr	Lys	Glu	Glu	Cys	Gln	Arg	Ile	Phe	Asp	Leu	Gln	Asn	Arg
1105					1110					1115					112
Val	Leu	Ala	Ser	Ser	Glu	Val	Leu	Ser	Thr	Asp	Glu	Ala	Glu	Ser	Ser
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Ala	Ser	Glu	Glu	Ser	Asp	Leu	Glu	Glu	Leu	Gly	Lys	Asn	Leu	Glu	Asn
			1140					1145					1150		
Met	Leu	Ser	Asn	Lys	Lys	Thr	Ser	Thr	Gln	Leu	Ser	Arg	Glu	Arg	Glu
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Glu	Leu	Glu	Arg	Gln	Glu	Leu	Leu	Arg	Gln	Leu	Asp	Glu	Glu	His	Gly	
1170					1175					1180						
Gly	Pro	Ser	Gly	Ser	Gly	Gly	Ala	Lys	Gly	Ala	Lys	Gly	Lys	Asp	Asp	
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Pro	Gly	Gln	Gln	Met	Leu	Ala	Thr	Asn	Asn	Gln	Gly	Arg	Ile	Leu	Arg	
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Ile	Thr	Arg	Thr	Phe	Arg	Gly	Asn	Asp	Gly	Lys	Glu	Tyr	Thr	Arg	Val	
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Glu	Thr	Val	Arg	Arg	Gln	Pro	Val	Ile	Asp	Ala	Tyr	Ile	Lys	Ile	Arg	
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Thr	Thr	Lys	Asp	Glu	Gln	Phe	Ile	Lys	Gln	Phe	Ala	Thr	Leu	Asp	Glu	
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Leu	Arg	Arg	Ile	Lys	Arg	Asn	Gln	Glu	Arg	Glu	Arg	Leu	Ala	Gln	Leu	
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Ala	Gln	Asn	Gln	Lys	Leu	Gln	Pro	Gly	Gly	Met	Pro	Thr	Ser	Leu	Gly	
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Asp	Pro	Lys	Ser	Ser	Gly	Gly	His	Ser	His	Lys	Glu	Arg	Asp	Ser	Gly	
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Tyr	Lys	Glu	Val	Ser	Pro	Ser	Arg	Lys	Lys	Phe	Lys	Leu	Lys	Pro	Asp	
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Leu	Lys	Leu	Lys	Cys	Gly	Ala	Cys	Gly	Gln	Val	Gly	His	Met	Arg	Thr	
1345					1350					1355					136	
Asn	Lys	Ala	Cys	Pro	Leu	Tyr	Ser	Gly	Met	Gln	Ser	Ser	Leu	Ser	Gln	
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Ser	Asn	Pro	Ser	Leu	Ala	Asp	Asp	Phe	Asp	Glu	Gln	Ser	Glu	Lys	Glu	
		1380						1385						1390		
Met	Thr	Met	Asp	Asp	Asp	Asp	Leu	Val	Asn	Val	Asp	Gly	Thr	Lys	Val	
		1395					1400						1405			
Thr	Leu	Ser	Ser	Lys	Ile	Leu	Lys	Arg	His	Gly	Gly	Asp	Asp	Gly	Lys	
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Ala	Met	Gly	Lys	Lys	Lys	Arg	Arg	Val	Gly	Gly	Asp	Leu	His	Cys	Asp	
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Tyr	Leu	Gln	Arg	His	Asn	Lys	Thr	Ala	Asn	Arg	Arg	Arg	Thr	Asp	Pro	
		1460						1465						1470		
Val	Val	Val	Leu	Ser	Ser	Ile	Leu	Glu	Ile	Ile	His	Asn	Glu	Leu	Arg	
		1475					1480						1485			
Ser	Met	Pro	Asp	Val	Ser	Pro	Phe	Leu	Phe	Pro	Val	Ser	Ala	Lys	Lys	
	1490					1495					1500					
Val	Pro	Asp	Tyr	Tyr	Arg	Val	Val	Thr	Lys	Pro	Met	Asp	Leu	Gln	Thr	
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Met	Arg	Glu	Tyr	Ile	Arg	Gln	Arg	Arg	Tyr	Thr	Ser	Arg	Glu	Met	Phe	
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Leu	Glu	Asp	Leu	Lys	Gln	Ile	Val	Asp	Asn	Ser	Leu	Ile	Tyr	Asn	Gly	
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Pro	Gln	Ser	Ala	Tyr	Thr	Leu	Ala	Ala	Gln	Arg	Met	Phe	Ser	Ser	Cys	
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Phe	Glu	Leu	Leu	Ala	Glu	Arg	Glu	Asp	Lys	Leu	Met	Arg	Leu	Glu	Lys	
	1570					1575						1580				

Ala	Ile	Asn	Pro	Leu	Leu	Asp	Asp	Asp	Asp	Gln	Val	Ala	Leu	Ser	Phe	1585	1590	1595	160
Ile	Phe	Asp	Lys	Leu	His	Ser	Gln	Ile	Lys	Gln	Leu	Pro	Glu	Ser	Trp	1605	1610	1615	1615
Pro	Phe	Leu	Lys	Pro	Val	Asn	Lys	Lys	Gln	Val	Lys	Asp	Tyr	Tyr	Thr	1620	1625	1630	1630
Val	Ile	Lys	Arg	Pro	Met	Asp	Leu	Glu	Thr	Ile	Gly	Lys	Asn	Ile	Glu	1635	1640	1645	1645
Ala	His	Arg	Tyr	His	Ser	Arg	Ala	Glu	Tyr	Leu	Ala	Asp	Ile	Glu	Leu	1650	1655	1660	1660
Ile	Ala	Thr	Asn	Cys	Glu	Gln	Tyr	Asn	Gly	Ser	Asp	Thr	Arg	Tyr	Thr	1665	1670	1675	168
Lys	Phe	Ser	Lys	Lys	Ile	Leu	Glu	Tyr	Ala	Gln	Thr	Gln	Leu	Ile	Glu	1685	1690	1695	1695
Phe	Ser	Glu	His	Cys	Gly	Gln	Leu	Glu	Asn	Asn	Ile	Ala	Lys	Thr	Gln	1700	1705	1710	1710
Glu	Arg	Ala	Arg	Glu	Asn	Ala	Pro	Glu	Phe	Asp	Glu	Ala	Trp	Gly	Asn	1715	1720	1725	1725
Asp	Asp	Tyr	Asn	Phe	Asp	Arg	Gly	Ser	Arg	Ala	Ser	Ser	Pro	Gly	Asp	1730	1735	1740	1740
Asp	Tyr	Ile	Asp	Val	Glu	Gly	His	Gly	Gly	His	Ala	Ser	Ser	Ser	Asn	1745	1750	1755	176
Ser	Ile	His	Arg	Ser	Met	Gly	Ala	Glu	Ala	Gly	Ser	Ser	His	Thr	Ala	1765	1770	1775	1775
Pro	Ala	Val	Arg	Lys	Pro	Ala	Pro	Pro	Gly	Pro	Gly	Glu	Val	Lys	Arg	1780	1785	1790	1790
Gly	Arg	Gly	Arg	Pro	Arg	Lys	Gln	Arg	Asp	Pro	Val	Glu	Glu	Asp	Leu	1795	1800	1805	1805
Gln	Cys	Ser	Thr	Asp	Asp	Glu	Asp	Asp	Asp	Glu	Glu	Glu	Asp	Phe	Gln	1810	1815	1820	1820
Glu	Val	Ser	Glu	Asp	Glu	Asn	Asn	Ala	Ala	Ser	Ile	Leu	Asp	Gln	Gly	1825	1830	1835	184
Glu	Arg	Ile	Asn	Ala	Pro	Ala	Asp	Ala	Met	Asp	Gly	Met	Phe	Asp	Pro	1845	1850	1855	1855
Lys	Asn	Ile	Lys	Thr	Glu	Ile	Asp	Leu	Glu	Ala	His	Gln	Met	Ala	Asp	1860	1865	1870	1870
Glu	Ser	Met	Asp	Val	Asp	Pro	Asn	Tyr	Asp	Pro	Ser	Asp	Phe	Leu	Ala	1875	1880	1885	1885
Met	His	Lys	Gln	Arg	Gln	Ser	Leu	Gly	Glu	Pro	Ser	Ser	Leu	Gln	Gly	1890	1895	1900	1900
Ala	Phe	Thr	Asn	Phe	Leu	Ser	His	Glu	Gln	Asp	Asp	Asn	Gly	Pro	Tyr	1905	1910	1915	192
Asn	Pro	Ala	Glu	Ala	Ser	Thr	Ser	Ala	Ala	Ser	Gly	Ala	Asp	Leu	Gly	1925	1930	1935	1935
Met	Asp	Ala	Ser	Met	Ala	Met	Gln	Met	Ala	Pro	Glu	Met	Pro	Val	Asn	1940	1945	1950	1950
Thr	Met	Asn	Asn	Gly	Met	Gly	Ile	Asp	Asp	Asp	Leu	Asp	Ile	Ser	Glu	1955	1960	1965	1965
Ser	Asp	Glu	Glu	Asp	Asp	Gly	Ser	Arg	Val	Arg	Ile	Lys	Lys	Glu	Val	1970	1975	1980	1980
Phe	Asp	Asp	Gly	Asp	Tyr	Ala	Leu	Gln	His	Gln	Gln	Met	Gly	Gln	Ala	1985	1990	1995	200

Ala Ser Gln Ser Gln Ile Tyr Met Val Asp Ser Ser Asn Glu Pro Thr  
 2005 2010 2015  
 Thr Leu Asp Tyr Gln Gln Pro Pro Gln Leu Asp Phe Gln Gln Val Gln  
 2020 2025 2030  
 Glu Met Glu Gln Leu Gln His Gln Val Met Pro Pro Met Gln Ser Glu  
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 Gln Leu Gln Gln Gln Gln Thr Pro Gln Gly Asp Asn Asp Tyr Ala Trp  
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 Thr Phe  
 2065

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 <213> Homo sapiens

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 Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly  
 20 25 30  
 Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly  
 35 40 45  
 Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys  
 50 55 60  
 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu  
 65 70 75 80  
 Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn  
 85 90 95  
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp  
 100 105 110  
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met  
 115 120 125  
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr  
 130 135 140  
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro  
 145 150 155 160  
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr  
 165 170 175  
 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met  
 180 185 190  
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr  
 195 200 205  
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro  
 210 215 220  
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg  
 225 230 235 240  
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg  
 245 250 255  
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu  
 260 265 270  
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln



		275					280					285				
Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln	
	290					295					300					
Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys	
305					310					315					320	
Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro	
				325					330					335		
Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met	
			340					345					350			
Leu	Gly	Val	Pro	Glu	Asp	Gly	Ser	Gly	Phe	Asp	Tyr	Gly	Phe	Lys	Leu	
		355					360					365				
Arg	Lys	Thr	Glu	His	Glu	Pro	Val	Ile	Lys	Ser	Arg	Met	Ile	Glu	Glu	
	370					375					380					
Phe	Arg	Lys	Leu	Glu	Glu	Asn	Asn	Gly	Thr	Asp	Leu	Leu	Ala	Asp	Glu	
385					390					395					400	
Asn	Phe	Leu	Met	Val	Thr	Gln	Leu	His	Trp	Glu	Asp	Asp	Ile	Ile	Trp	
				405					410					415		
Asp	Gly	Glu	Asp	Val	Lys	His	Lys	Gly	Thr	Lys	Pro	Gln	Arg	Ala	Ser	
		420						425					430			
Leu	Ala	Gly	Trp	Leu	Pro	Ser	Ser	Met	Thr	Arg	Asn	Ala	Met	Ala	Tyr	
		435					440					445				
Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro	Trp	
	450					455					460					
Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg	Trp	
465					470					475					480	
Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu	Glu	
				485				490						495		
Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu	Glu	
		500						505					510			
Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys	Glu	
		515					520					525				
Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly	Lys	
	530					535					540					
Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro	Glu	
545					550					555					560	
Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys	
				565					570					575		
Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His	Ser	
			580					585					590			
Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met	Gly	
		595					600					605				
Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr	Ser	
	610					615					620					
Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu	Leu	
625					630					635					640	
Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln	Ala	
				645					650					655		
Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu	Thr	
		660						665					670			
Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn	Gly	
	675						680					685				
Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr	Tyr	

690		695		700
Lys Arg Lys Pro Gly	Lys Asp Pro Gly Ala	Pro Asp Cys Lys Tyr Gly		
705	710	715		720
Glu Thr Val Tyr Cys	His Thr Ser Pro Phe	Leu Gly Ser Leu His Pro		
	725	730		735
Gly Gln Leu Leu Gln	Ala Phe Glu Asn Asn	Leu Phe Arg Ala Pro Ile		
	740	745		750
Tyr Leu His Lys Met	Pro Glu Thr Asp Phe	Leu Ile Ile Arg Thr Arg		
	755	760		765
Gln Gly Tyr Tyr Ile	Arg Glu Leu Val Asp	Ile Phe Val Val Gly Gln		
	770	775		780
Gln Cys Pro Leu Phe	Glu Val Pro Gly Pro	Asn Ser Lys Arg Ala Asn		
785	790	795		800
Thr His Ile Arg Asp	Phe Leu Gln Val Phe	Ile Tyr Arg Leu Phe Trp		
	805	810		815
Lys Ser Lys Asp Arg	Pro Arg Arg Ile Arg	Met Glu Asp Ile Lys Lys		
	820	825		830
Ala Phe Pro Ser His	Ser Glu Ser Ser Ile	Arg Lys Arg Leu Lys Leu		
	835	840		845
Cys Ala Asp Phe Lys	Arg Thr Gly Met Asp	Ser Asn Trp Trp Val Leu		
	850	855		860
Lys Ser Asp Phe Arg	Leu Pro Thr Glu Glu	Glu Ile Arg Ala Met Val		
865	870	875		880
Ser Pro Glu Gln Cys	Cys Ala Tyr Tyr Ser	Met Ile Ala Ala Glu Gln		
	885	890		895
Arg Leu Lys Asp Ala	Gly Tyr Gly Glu Lys	Ser Phe Phe Ala Pro Glu		
	900	905		910
Glu Glu Asn Glu Glu	Asp Phe Gln Met Lys	Ile Asp Asp Glu Val Arg		
	915	920		925
Thr Ala Pro Trp Asn	Thr Thr Arg Ala Phe	Ile Ala Ala Met Lys Gly		
	930	935		940
Lys Cys Leu Leu Glu	Val Thr Gly Val Ala	Asp Pro Thr Gly Cys Gly		
945	950	955		960
Glu Gly Phe Ser Tyr	Val Lys Ile Pro Asn	Lys Pro Thr Gln Gln Lys		
	965	970		975
Asp Asp Lys Glu Pro	Gln Pro Val Lys Thr	Val Thr Gly Thr Asp		
	980	985		990
Ala Asp Leu Arg Arg	Leu Ser Leu Lys Asn	Ala Lys Gln Leu Leu Arg		
	995	1000		1005
Lys Phe Gly Val Pro	Glu Glu Glu Ile Lys	Lys Leu Ser Arg Trp Glu		
	1010	1015		1020
Val Ile Asp Val Val	Arg Thr Met Ser Thr	Glu Gln Ala Arg Ser Gly		
1025	1030	1035		104
Glu Gly Pro Met Ser	Lys Phe Ala Arg Gly	Ser Arg Phe Ser Val Ala		
	1045	1050		1055
Glu His Gln Glu Arg	Tyr Lys Glu Glu Cys	Gln Arg Ile Phe Asp Leu		
	1060	1065		1070
Gln Asn Lys Val Leu	Ser Ser Thr Glu Val	Leu Ser Thr Asp Thr Asp		
	1075	1080		1085
Ser Ser Ser Ala Glu	Asp Ser Asp Phe Glu	Glu Met Gly Lys Asn Ile		
	1090	1095		1100
Glu Asn Met Leu Gln	Asn Lys Lys Thr Ser	Ser Gln Leu Ser Arg Glu		

1105		1110		1115		112
Arg Glu Glu Gln Glu	Arg Lys Glu Leu Gln	Arg Met Leu Leu Ala Ala				
	1125		1130		1135	
Gly Ser Ala Ala Ser	Gly Asn Asn His Arg	Asp Asp Asp Thr Ala Ser				
	1140		1145		1150	
Val Thr Ser Leu Asn Ser	Ser Ala Thr Gly Arg	Cys Leu Lys Ile Tyr				
	1155		1160		1165	
Arg Thr Phe Arg Asp	Glu Glu Gly Lys Glu Tyr	Val Arg Cys Glu Thr				
	1170		1175		1180	
Val Arg Lys Pro Ala Val	Ile Asp Ala Tyr Val	Arg Ile Arg Thr Thr				
	1185		1190		1195	120
Lys Asp Glu Glu Phe Ile	Arg Lys Phe Ala Leu	Phe Asp Glu Gln His				
	1205		1210		1215	
Arg Glu Glu Met Arg	Lys Glu Arg Arg Arg	Ile Gln Glu Gln Leu Arg				
	1220		1225		1230	
Arg Leu Lys Arg Asn	Gln Glu Lys Glu Lys	Leu Lys Gly Pro Pro Glu				
	1235		1240		1245	
Lys Lys Pro Lys Lys	Met Lys Glu Arg Pro	Asp Leu Lys Leu Lys Cys				
	1250		1255		1260	
Gly Ala Cys Gly Ala Ile	Gly His Met Arg Thr	Asn Lys Phe Cys Pro				
	1265		1270		1275	128
Leu Tyr Tyr Gln Thr	Asn Ala Pro Pro Ser	Asn Pro Val Ala Met Thr				
	1285		1290		1295	
Glu Glu Gln Glu Glu	Glu Leu Glu Lys Thr	Val Ile His Asn Asp Asn				
	1300		1305		1310	
Glu Glu Leu Ile Lys	Val Glu Gly Thr Lys	Ile Val Leu Gly Lys Gln				
	1315		1320		1325	
Leu Ile Glu Ser Ala Asp	Glu Val Arg Arg Lys	Ser Leu Val Leu Lys				
	1330		1335		1340	
Phe Pro Lys Gln Gln	Leu Pro Pro Lys Lys	Lys Arg Val Gly Thr				
	1345		1350		1355	136
Thr Val His Cys Asp	Tyr Leu Asn Arg Pro	His Lys Ser Ile His Arg				
	1365		1370		1375	
Arg Arg Thr Asp	Pro Met Val Thr	Leu Ser Ser Ile Leu Glu Ser Ile				
	1380		1385		1390	
Ile Asn Asp Met Arg	Asp Leu Pro Asn Thr	Tyr Pro Phe His Thr Pro				
	1395		1400		1405	
Val Asn Ala Lys Val	Val Lys Asp Tyr Tyr	Lys Ile Ile Thr Arg Pro				
	1410		1415		1420	
Met Asp Leu Gln Thr	Leu Arg Glu Asn Val	Arg Lys Arg Leu Tyr Pro				
	1425		1430		1435	144
Ser Arg Glu Glu Phe	Arg Glu His Leu Glu	Leu Ile Val Lys Asn Ser				
	1445		1450		1455	
Ala Thr Tyr Asn Gly	Pro Lys His Ser	Leu Thr Gln Ile Ser Gln Ser				
	1460		1465		1470	
Met Leu Asp Leu Cys	Asp Glu Lys Leu Lys	Glu Lys Glu Asp Lys Leu				
	1475		1480		1485	
Ala Arg Leu Glu Lys	Ala Ile Asn Pro Leu	Leu Asp Asp Asp Asp Gln				
	1490		1495		1500	
Val Ala Phe Ser Phe	Ile Leu Asp Asn Ile	Val Thr Gln Lys Met Met				
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Ala Val Pro Asp Ser	Trp Pro Phe His His	Pro Val Asn Lys Lys Phe				

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Val	Pro	Asp	Tyr	Tyr	Lys	Val	Ile	Val	Asn	Pro	Met	Asp	Leu	Glu	Thr				
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Ile	Arg	Lys	Asn	Ile	Ser	Lys	His	Lys	Tyr	Gln	Ser	Arg	Glu	Ser	Phe				
		1555					1560					1565							
Leu	Asp	Asp	Val	Asn	Leu	Ile	Leu	Ala	Asn	Ser	Val	Lys	Tyr	Asn	Gly				
	1570					1575					1580								
Pro	Glu	Ser	Gln	Tyr	Thr	Lys	Thr	Ala	Gln	Glu	Ile	Val	Asn	Val	Cys				
1585					1590					1595					160				
Tyr	Gln	Thr	Leu	Thr	Glu	Tyr	Asp	Glu	His	Leu	Thr	Gln	Leu	Glu	Lys				
			1605						1610					1615					
Asp	Ile	Cys	Thr	Ala	Lys	Glu	Ala	Ala	Leu	Glu	Glu	Ala	Glu	Leu	Glu				
	1620						1625					1630							
Ser	Leu	Asp	Pro	Met	Thr	Pro	Gly	Pro	Tyr	Thr	Pro	Gln	Pro	Pro	Asp				
	1635						1640					1645							
Leu	Tyr	Asp	Thr	Asn	Thr	Ser	Leu	Ser	Met	Ser	Arg	Asp	Ala	Ser	Val				
	1650				1655						1660								
Phe	Gln	Asp	Glu	Ser	Asn	Met	Ser	Val	Leu	Asp	Ile	Pro	Ser	Ala	Thr				
1665					1670					1675					168				
Pro	Glu	Lys	Gln	Val	Thr	Gln	Glu	Gly	Glu	Asp	Gly	Asp	Gly	Asp	Leu				
			1685						1690					1695					
Ala	Asp	Glu	Glu	Glu	Gly	Thr	Val	Gln	Gln	Pro	Gln	Ala	Ser	Val	Leu				
	1700							1705				1710							
Tyr	Glu	Asp	Leu	Leu	Met	Ser	Glu	Gly	Glu	Asp	Asp	Glu	Glu	Asp	Ala				
	1715						1720					1725							
Gly	Ser	Asp	Glu	Glu	Gly	Asp	Asn	Pro	Phe	Ser	Ala	Ile	Gln	Leu	Ser				
	1730				1735						1740								
Glu	Ser	Gly	Ser	Asp	Ser	Asp	Val	Gly	Ser	Gly	Gly	Ile	Arg	Pro	Lys				
1745					1750					1755					176				
Gln	Pro	Arg	Met	Leu	Gln	Glu	Asn	Thr	Arg	Met	Asp	Met	Glu	Asn	Glu				
			1765						1770					1775					
Glu	Ser	Met	Met	Ser	Tyr	Glu	Gly	Asp	Gly	Gly	Glu	Ala	Ser	His	Gly				
	1780						1785					1790							
Leu	Glu	Asp	Ser	Asn	Ile	Ser	Tyr	Gly	Ser	Tyr	Glu	Glu	Pro	Asp	Pro				
	1795						1800					1805							
Lys	Ser	Asn	Thr	Gln	Asp	Thr	Ser	Phe	Ser	Ser	Ile	Gly	Gly	Tyr	Glu				
	1810					1815					1820								
Val	Ser	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Gln	Arg	Ser	Gly				
1825					1830					1835					184				
Pro	Ser	Val	Leu	Ser	Gln	Val	His	Leu	Ser	Glu	Asp	Glu	Glu	Asp	Ser				
			1845						1850					1855					
Glu	Asp	Phe	His	Ser	Ile	Ala	Gly	Asp	Ser	Asp	Leu	Asp	Ser	Asp	Glu				
		1860						1865					1870						

<210> 7

<211> 429

<212> PRT

<213> C. albicans

<400> 7

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Lys	Ile	Glu	Asn	Asp	Asn	Thr	Thr	Asn	Asn	Tyr	Asn	Gln	Asn	Asn	Ser	
			20					25					30			
Asn	Val	Gln	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Ile	Phe	Asn	Gly	Gln	Ile	
		35					40					45				
Asn	Leu	Asp	Lys	Leu	Lys	Leu	Asp	Met	Asn	Asp	Pro	Asn	Leu	Leu	Phe	
	50					55					60					
Val	Pro	Ser	Lys	Lys	Val	Asp	Ala	Thr	Lys	Ser	Val	Val	Pro	Ser	Thr	
65					70					75					80	
Asp	Lys	Leu	Leu	Glu	Leu	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Gln	Glu	Tyr	
				85					90					95		
Glu	Leu	Leu	Arg	Lys	Asn	Tyr	Asn	Thr	Lys	Gln	Arg	Ser	Gln	Leu	Ser	
			100					105					110			
Asn	Leu	Asn	Ile	Glu	His	Ser	Val	Pro	Ala	Leu	Arg	Leu	Gln	Thr	Pro	
		115					120					125				
Tyr	Tyr	Lys	Val	Lys	Leu	Ser	Thr	Asp	Glu	Thr	Arg	Ser	Phe	His	Arg	
	130					135					140					
Pro	Val	Phe	Asn	Val	Arg	Pro	Gly	Thr	Leu	Val	Ser	Phe	Ser	Lys	Leu	
145					150					155					160	
Lys	Leu	Arg	Lys	Arg	Lys	Lys	Asp	Lys	Gly	Lys	Ser	Leu	Gln	Gln	Ile	
				165					170					175		
Phe	Ser	Lys	Thr	Ser	Asp	Leu	Thr	Val	Ala	Asp	Thr	Gly	Asn	Ile	Ile	
			180					185					190			
Ala	Leu	Glu	Tyr	Ser	Glu	Gln	Tyr	Pro	Pro	Ile	Leu	Ser	Asn	Phe	Gly	
		195					200					205				
Met	Gly	Ser	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Glu	Arg	Pro	Asn	Asp	
	210					215					220					
Thr	Ser	Arg	Pro	Lys	Ala	Gln	Ile	Gly	Glu	Thr	His	Ile	Leu	Gly	Val	
225					230					235					240	
Glu	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Glu	Val	Ala	Pro	Gly	Asp	
				245					250					255		
Phe	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Val	Arg	Ala	Pro	Ile	Phe	Lys	
			260					265				270				
His	Asp	Asn	Lys	Pro	Thr	Asp	Phe	Leu	Leu	Val	Lys	Ser	Gln	Gly	Ala	
		275					280					285				
Gly	Ser	His	Gln	Lys	Phe	Tyr	Leu	Arg	Gly	Ile	Asn	Phe	Asn	Phe	Ala	
	290					295					300					
Val	Gly	Asn	Thr	Phe	Pro	Val	Glu	Val	Pro	Ala	Pro	His	Ser	Arg	Lys	
305					310					315					320	
Val	Thr	Asn	Ile	Ser	Lys	Asn	Arg	Leu	Lys	Met	Val	Val	Phe	Arg	Val	
				325					330					335		
Met	Asn	Ser	Leu	Gly	Val	Pro	Arg	Ile	Ser	Val	Lys	Asp	Val	Ser	Lys	
			340					345					350			
His	Phe	Pro	Glu	His	Ser	Asp	Met	Gln	Asn	Arg	Gln	Arg	Leu	Lys	Glu	
		355					360					365				
Phe	Met	Glu	Tyr	Gln	Arg	Gln	Gly	Glu	Asp	Gln	Gly	Tyr	Trp	Lys	Val	
	370					375					380					
Arg	Gly	Leu	Asn	Asp	Val	Ile	Pro	Gly	Glu	Glu	Glu	Ile	Arg	Thr	Met	
385					390					395					400	
Ile	Thr	Pro	Glu	Asp	Ser	Ser	Leu	Met	Asp	Thr	Met	Gln	Phe	Gly	Gln	
				405					410					415		
Gln	Val	Leu	Asp	Asp	Asn	Met	Val	Leu	Phe	Gly	Glu	Gln				
			420					425								

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 <211> 434  
 <212> PRT  
 <213> S. cerevisiae

<400> 8

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			20					25					30		
Asp	Ala	Lys	Leu	Lys	Glu	Ser	Lys	His	Ala	Glu	Leu	Asn	Met	Asn	Asp
		35					40					45			
Glu	Lys	Leu	Leu	Leu	Met	Ile	Glu	Lys	Thr	Asn	Asn	Leu	Ala	Gln	Gln
	50					55					60				
Lys	Gln	Gln	Leu	Asp	Ser	Ser	Asn	Leu	Ile	Leu	Pro	Leu	Asn	Glu	Thr
65				70						75				80	
Ile	Leu	Gln	Gln	Lys	Phe	Asn	Leu	Ser	Asn	Asp	Asp	Lys	Tyr	Gln	Ile
				85					90					95	
Leu	Lys	Lys	Thr	His	Gln	Thr	Lys	Val	Arg	Ser	Thr	Ile	Ser	Asn	Leu
			100					105					110		
Asn	Ile	Gln	His	Ser	Gln	Pro	Ala	Ile	Asn	Leu	Gln	Ser	Pro	Phe	Tyr
		115					120					125			
Lys	Val	Ala	Val	Pro	Arg	Tyr	Gln	Leu	Arg	His	Phe	His	Arg	Glu	Asn
	130					135					140				
Phe	Gly	Ser	His	Ile	Arg	Pro	Gly	Thr	Lys	Ile	Val	Phe	Ser	Lys	Leu
145				150						155					160
Lys	Ala	Arg	Lys	Arg	Lys	Arg	Asp	Lys	Gly	Lys	Asp	Val	Lys	Glu	Ser
				165					170					175	
Phe	Ser	Thr	Ser	Gln	Asp	Leu	Thr	Ile	Gly	Asp	Thr	Ala	Pro	Val	Tyr
			180					185					190		
Leu	Met	Glu	Tyr	Ser	Glu	Gln	Thr	Pro	Val	Ala	Leu	Ser	Lys	Phe	Gly
	195						200					205			
Met	Ala	Asn	Lys	Leu	Ile	Asn	Tyr	Tyr	Arg	Lys	Ala	Asn	Glu	Gln	Asp
	210					215					220				
Thr	Leu	Arg	Pro	Lys	Leu	Pro	Val	Gly	Glu	Thr	His	Val	Leu	Gly	Val
225				230						235					240
Gln	Asp	Lys	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Phe	Val	Glu	Pro	Gly	His
				245					250					255	
Ile	Val	Pro	Thr	Leu	Tyr	Asn	Asn	Met	Ile	Arg	Ala	Pro	Val	Phe	Lys
			260					265					270		
His	Asp	Ile	Ser	Gly	Thr	Asp	Phe	Leu	Leu	Thr	Lys	Ser	Ser	Gly	Phe
		275					280					285			
Gly	Ile	Ser	Asn	Arg	Phe	Tyr	Leu	Arg	Asn	Ile	Asn	His	Leu	Phe	Thr
	290					295					300				
Val	Gly	Gln	Thr	Phe	Pro	Val	Glu	Glu	Ile	Pro	Gly	Pro	Asn	Ser	Arg
305				310						315					320
Lys	Val	Thr	Ser	Met	Lys	Ala	Thr	Arg	Leu	Lys	Met	Ile	Ile	Tyr	Arg
				325					330					335	
Ile	Leu	Asn	His	Asn	His	Ser	Lys	Ala	Ile	Ser	Ile	Asp	Pro	Ile	Ala
			340					345					350		
Lys	His	Phe	Pro	Asp	Gln	Asp	Tyr	Gly	Gln	Asn	Arg	Gln	Lys	Val	Lys
		355					360					365			

Glu	Phe	Met	Lys	Tyr	Gln	Arg	Asp	Gly	Pro	Glu	Lys	Gly	Leu	Trp	Arg
	370					375					380				
Leu	Lys	Asp	Asp	Glu	Lys	Leu	Leu	Asp	Asn	Glu	Ala	Val	Lys	Ser	Leu
385					390					395					400
Ile	Thr	Pro	Glu	Gln	Ile	Ser	Gln	Val	Glu	Ser	Met	Ser	Gln	Gly	Leu
				405					410					415	
Gln	Phe	Gln	Glu	Asp	Asn	Glu	Ala	Tyr	Asn	Phe	Asp	Ser	Lys	Leu	Lys
			420					425					430		
Ser	Leu														

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 <211> 415  
 <212> PRT  
 <213> S. pombe

<400> 9															
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Asp	Ile	Asp	Phe	Ala	Phe	Asp	Glu	Asn	Ile	Phe	Asp	Gly	Asp	Thr	Gly
			20					25					30		
Thr	Ser	Lys	Val	Val	Leu	Asn	Leu	Asn	Asp	Pro	Lys	Leu	Leu	Leu	Gln
		35				40						45			
Pro	Gln	Leu	Pro	Lys	Lys	Glu	Asp	Ser	Gln	Arg	Ser	Phe	Ala	Asp	Thr
	50					55					60				
His	Gln	Arg	Asn	Ser	Leu	Ala	Trp	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Pro
65					70					75					80
Ala	Tyr	Glu	Met	Leu	Lys	Gln	Asn	His	Gln	Ser	Lys	Val	Arg	Asn	Thr
			85						90					95	
Leu	Ser	Gln	Leu	Ala	Ile	Glu	His	Ala	Ala	Phe	Ala	Glu	Lys	Leu	Thr
			100					105					110		
Phe	Pro	Tyr	Tyr	Lys	Thr	Arg	Leu	Ser	Lys	Arg	Ala	Val	Arg	Ser	Tyr
	115						120					125			
His	Arg	Pro	Thr	Met	Ser	Phe	Lys	Pro	Asn	Ala	Ala	Ile	Val	Phe	Ser
	130					135					140				
Pro	Leu	Ile	Val	Arg	Lys	Arg	Ser	Lys	Asp	Lys	His	Lys	Ser	Glu	Arg
145					150					155					160
Glu	Leu	Ile	Pro	Thr	Thr	Lys	Glu	Ile	Thr	Met	Gly	Asp	Thr	Thr	His
				165					170					175	
Ala	Ile	Leu	Val	Glu	Phe	Ser	Glu	Glu	His	Pro	Ala	Val	Leu	Ser	Asn
			180					185					190		
Ala	Gly	Met	Ala	Ser	Arg	Ile	Val	Asn	Tyr	Tyr	Arg	Lys	Lys	Asn	Glu
	195						200					205			
Gln	Asp	Glu	Ser	Arg	Pro	Lys	Leu	Glu	Val	Gly	Glu	Ser	His	Val	Leu
	210					215					220				
Asp	Val	Gln	Asp	Arg	Ser	Pro	Phe	Trp	Asn	Phe	Gly	Ser	Val	Glu	Pro
225					230					235					240
Gly	Glu	Ile	Thr	Pro	Thr	Leu	Tyr	Asn	Lys	Met	Ile	Arg	Ala	Pro	Leu
				245					250					255	
Phe	Lys	His	Glu	Val	Pro	Pro	Thr	Asp	Phe	Ile	Leu	Ile	Arg	Asn	Ser
			260					265					270		
Ser	Ser	Tyr	Gly	Ser	Lys	Tyr	Tyr	Leu	Lys	Asn	Ile	Asn	His	Met	Phe

		275					280			285					
Val	Ser	Gly	Gln	Thr	Phe	Pro	Val	Thr	Asp	Val	Pro	Gly	Pro	His	Ser
	290					295					300				
Arg	Lys	Val	Thr	Thr	Ala	Ser	Lys	Asn	Arg	Leu	Lys	Met	Leu	Val	Phe
305					310					315					320
Arg	Leu	Ile	Arg	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Ile	Arg	Gln	Leu
				325					330					335	
Ser	Lys	His	Phe	Ser	Asp	Gln	Asn	Glu	Met	Gln	Ile	Arg	Gln	Arg	Leu
			340					345					350		
Lys	Glu	Phe	Met	Glu	Tyr	Lys	Lys	Lys	Gly	Asp	Gly	Pro	Gly	Tyr	Trp
		355				360						365			
Lys	Leu	Lys	Ser	Asn	Glu	Val	Val	Pro	Asp	Glu	Ala	Gly	Thr	Arg	Ser
	370					375					380				
Met	Val	Ser	Pro	Glu	Thr	Val	Cys	Leu	Leu	Glu	Ser	Met	Gln	Val	Gly
385					390					395					400
Val	Arg	Gln	Leu	Glu	Asp	Ala	Gly	Tyr	Gly	Lys	Thr	Met	Asp	Glu	
				405					410					415	

<210> 10  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

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Tyr	Asn	Val	Gln	Gln	Gly	Phe	Ala	Ala	Thr	Leu	Asp	Asp	Asp	Lys	Pro
			20					25					30		
Trp	Tyr	Ser	Ile	Phe	Pro	Ile	Asp	Asn	Glu	Asp	Leu	Val	Tyr	Gly	Arg
		35					40					45			
Trp	Glu	Asp	Asn	Ile	Ile	Trp	Asp	Ala	Gln	Ala	Met	Pro	Arg	Leu	Leu
	50					55					60				
Glu	Pro	Pro	Val	Leu	Thr	Leu	Asp	Pro	Asn	Asp	Glu	Asn	Leu	Ile	Leu
65					70					75					80
Glu	Ile	Pro	Asp	Glu	Lys	Glu	Glu	Ala	Thr	Ser	Asn	Ser	Pro	Ser	Lys
			85						90					95	
Glu	Ser	Lys	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Ser	Arg	Ile	Leu	Leu	Gly
			100					105					110		
Lys	Thr	Gly	Val	Ile	Lys	Glu	Glu	Pro	Gln	Gln	Asn	Met	Ser	Gln	Pro
		115					120					125			
Glu	Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro
	130					135					140				
Lys	Gln	Gln	Gly	Leu	Arg	Gly	Thr	Phe	Gly	Gly	Asn	Ile	Ile	Gln	His
145					150					155					160
Ser	Ile	Pro	Ala	Val	Glu	Leu	Arg	Gln	Pro	Phe	Phe	Pro	Thr	His	Met
			165						170					175	
Gly	Pro	Ile	Lys	Leu	Arg	Gln	Phe	His	Arg	Pro	Pro	Leu	Lys	Lys	Tyr
			180					185					190		
Ser	Phe	Gly	Ala	Leu	Ser	Gln	Pro	Gly	Pro	His	Ser	Val	Gln	Pro	Leu
	195					200						205			
Leu	Lys	His	Ile	Lys	Lys	Lys	Ala	Lys	Met	Arg	Glu	Gln	Glu	Arg	Gln
	210					215					220				



Ala	Ser	Gly	Gly	Gly	Glu	Met	Phe	Phe	Met	Arg	Thr	Pro	Gln	Asp	Leu
225					230					235					240
Thr	Gly	Lys	Asp	Gly	Asp	Leu	Ile	Leu	Ala	Glu	Tyr	Ser	Glu	Glu	Asn
				245					250					255	
Gly	Pro	Leu	Met	Met	Gln	Val	Gly	Met	Ala	Thr	Lys	Ile	Lys	Asn	Tyr
			260					265					270		
Tyr	Lys	Arg	Lys	Pro	Gly	Lys	Asp	Pro	Gly	Ala	Pro	Asp	Cys	Lys	Tyr
		275					280					285			
Gly	Glu	Thr	Val	Tyr	Cys	His	Thr	Ser	Pro	Phe	Leu	Gly	Ser	Leu	His
	290					295					300				
Pro	Gly	Gln	Leu	Leu	Gln	Ala	Phe	Glu	Asn	Asn	Leu	Phe	Arg	Ala	Pro
305					310				315						320
Ile	Tyr	Leu	His	Lys	Met	Pro	Glu	Thr	Asp	Phe	Leu	Ile	Ile	Arg	Thr
				325					330					335	
Arg	Gln	Gly	Tyr	Tyr	Ile	Arg	Glu	Leu	Val	Asp	Ile	Phe	Val	Val	Gly
			340					345					350		
Gln	Gln	Cys	Pro	Leu	Phe	Glu	Val	Pro	Gly	Pro	Asn	Ser	Lys	Arg	Ala
		355					360					365			
Asn	Thr	His	Ile	Arg	Asp	Phe	Leu	Gln	Val	Phe	Ile	Tyr	Arg	Leu	Phe
	370					375					380				
Trp	Lys	Ser	Lys	Asp	Arg	Pro	Arg	Arg	Ile	Arg	Met	Glu	Asp	Ile	Lys
385				390						395					400
Lys	Ala	Phe	Pro	Ser	His	Ser	Glu	Ser	Ser	Ile	Arg	Lys	Arg	Leu	Lys
				405					410					415	
Leu	Cys	Ala	Asp	Phe	Lys	Arg	Thr	Gly	Met	Asp	Ser	Asn	Trp	Trp	Val
			420					425					430		
Leu	Lys	Ser	Asp	Phe	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Ile	Arg	Ala	Met
		435					440					445			
Val	Ser	Pro	Glu	Gln	Cys	Cys	Ala	Tyr	Tyr	Ser	Met	Ile	Ala	Ala	Glu
	450				455						460				
Gln	Arg	Leu	Lys	Asp	Ala	Gly	Tyr	Gly	Glu	Lys	Ser	Phe	Phe	Ala	Pro
465					470					475					480
Glu															

<210> 11  
 <211> 74  
 <212> PRT  
 <213> C. albicans

<400> 11															
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Glu	Lys	Glu	Lys	Glu	Gln	Glu	Arg	Glu	Glu	Glu	Lys	Gly	Lys	Asp	Lys
			20					25					30		
Glu	Lys	Asp	Lys	Asp	Lys	Glu	Lys	Asp	Lys	Thr	Glu	Lys	Glu	Lys	Ser
		35					40					45			
Lys	Lys	Ser	Lys	Glu	Gln	Asp	Thr	Glu	Ile	Asp	Val	Glu	Glu	Glu	Leu
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Ala	Pro	Trp	Asn	Leu	Ser	Arg	Asn	Phe	Val						
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 <212> DNA  
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 <223> sequence source: Degenerate oligonucleotide designed and used  
 to amplify fragments of DNA from *Candida albicans* strain SC5314 genomic  
 DNA by polymerase chain reaction. n is defined as Inosine.

<400> 12  
 ccwggwccwa aytcnadd 18

<210> 13  
 <211> 23  
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 to amplify fragments of DNA from *Candida albicans* strain SC5314 genomic  
 DNA by polymerase chain reaction.

<400> 13  
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<210> 14  
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 <220>  
 <223> sequence source: Degenerate oligonucleotide designed and used  
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 DNA by polymerase chain reaction.

<400> 14  
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<210> 15  
 <211> 19  
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 used to amplify fragments of DNA from *Candida albicans* strain SC5314  
 genomic DNA by polymerase chain reaction. n is defined as Inosine.

<400> 15  
 ttrtthcayc tnartgwcc 19

<210> 16  
 <211> 30  
 <212> DNA  
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<220>  
 <223> S. cerevisiae  
  
 <400> 16  
 ccgctcgaga tgacacccaa cttaaagttc 30  
  
 <210> 17  
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 <212> DNA  
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 <223> S. cerevisiae  
  
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 cgcggatcca gagatttttag cttagaatc 29  
  
 <210> 18  
 <211> 37  
 <212> DNA  
 <213> "Artificial Sequence"  
 <220>  
 <223> C. albicans  
 <400> 18  
 ggaattccat atgcttttgc tcaacaatcc cttggac 37  
  
 <210> 19  
 <211> 32  
 <212> DNA  
 <213> "Artificial Sequence"  
 <220>  
 <223> C. albicans  
 <400> 19  
 cgcggatccc tgctctgctc accgaataac ac 32  
  
 <210> 20  
 <211> 37  
 <212> DNA  
 <213> "Artificial Sequence"  
 <220>  
 <223> Homo sapiens  
  
 <400> 20  
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 <210> 21  
 <211> 33  
 <212> DNA  
 <213> "Artificial Sequence"  
 <220>  
 <223> Homo sapiens  
 <400> 21  
 ccgctcgagt tctggagcaa aaaaggattt ctc 33

<210> 22  
 <211> 0  
 <212> DNA  
 <213> Homo sapiens

<400> 22

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Phe	Leu	Arg	Leu	Phe	Gly	Pro	Gly	Lys	Asn	Val	Pro	Ser	Val	Trp	Arg
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Lys	Ser	Leu	Trp	Asn	Tyr	Asp	Tyr	Ala	Pro	Pro	Pro	Pro	Pro	Glu	Gln
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Cys	Leu	Ser	Asp	Asp	Glu	Ile	Thr	Met	Met	Ala	Pro	Val	Glu	Ser	Lys
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Phe	Ser	Gln	Ser	Thr	Gly	Asp	Ile	Asp	Lys	Val	Thr	Asp	Thr	Lys	Pro
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Arg	Val	Ala	Glu	Trp	Arg	Tyr	Gly	Pro	Ala	Arg	Leu	Trp	Tyr	Asp	Met
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Val	Lys	Asp	Pro	Trp	Asn	Leu	Ser	Asn	Asp	Glu	Tyr	Tyr	Tyr	Pro	Lys
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Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His  
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